

SEQUENCE LISTING

<110> Fujisawa Pharmaceutical Co., Ltd.

<120> A GENE CODING A CYCLIC LOPOPEPTIDE ACYLASE AND AN EXPRESSION  
THEREOF

<130> 09368

<150> JP 11-189644

<151> 1999-7-2

<160> 57

<210> 1

<211> 5692

<212> DNA

<213> Streptomyces Sp.

<220>

<221> CDS

<222> (948).. (3362)

<400> 1

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cggcagggag tgcacgggcc ggtcggtcgc ggcgaggccg agcgcggtga tcgcgctgac   240
gtactcgtgg accagggccc cgtgcgtcat catcgcgccc ttgggcaggg cggttggtccc   300
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 gagtccggcg gggagccgcc cggcgaggtc cgggtcggtc aggacgaggg aggagccgga 480  
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 gagaccggcc cgtgcgcagg cgaggaagcc gatcagatag gcgtcggagt tgtgcgcgta 600  
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Leu Thr Leu

cgc aac cgt ctg aga ctg ctc ggg gtc gcc ggt ctc gcc ctg ttc acc 1004  
 Arg Asn Arg Leu Arg Leu Leu Gly Val Ala Gly Leu Ala Leu Phe Thr

-35

-30

-25

gtg tcg gcg tcg ctg ccg cct gcc acc gcg tcc ggg acc cag gag acg 1052  
 Val Ser Ala Ser Leu Pro Pro Ala Thr Ala Ser Gly Thr Gln Glu Thr

-20

-15

-10

-5

cgg cac ccg tcc ggg agc ggt ctt tcg gcc gtc atc cgg tac acg gag 1100  
 Arg His Pro Ser Gly Ser Gly Leu Ser Ala Val Ile Arg Tyr Thr Glu

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5

10

tac ggc att ccg cac atc gtg gcg gag gac tac gcg cag ttg ggc ttc 1148  
 Tyr Gly Ile Pro His Ile Val Ala Glu Asp Tyr Ala Gln Leu Gly Phe

15

20

25

ggc acc ggc tgg gcg cag gcc gcc gat cag gtg tgc acg ctg gcg gac 1196  
 Gly Thr Gly Trp Ala Gln Ala Ala Asp Gln Val Cys Thr Leu Ala Asp

30	35	40	
ggc ttc ctc acg gtg cgc ggg gag cgg tgc agg ttc ttc ggc ccg gac			1244
Gly Phe Leu Thr Val Arg Gly Glu Arg Ser Arg Phe Phe Gly Pro Asp			
45	50	55	60
gcc gcc acg gac tac tcc ctc tcc tgc gcg gcg acg aac ctc tcc agc			1292
Ala Ala Thr Asp Tyr Ser Leu Ser Ser Ala Ala Thr Asn Leu Ser Ser			
	65	70	75
gac ctg tac ttc cgg ggc gtc cgc gac agc ggc acg gtg gag aag ctg			1340
Asp Leu Tyr Phe Arg Gly Val Arg Asp Ser Gly Thr Val Glu Lys Leu			
	80	85	90
ctc aag gag ccc gcg ccc gcc ggt ccg agc agg gac gtc aag gag acg			1388
Leu Lys Glu Pro Ala Pro Ala Gly Pro Ser Arg Asp Val Lys Glu Thr			
	95	100	105
atg cgc ggg ttc gcc gcc ggg tac aac gcg tgg atc gcg cag aac cgg			1436
Met Arg Gly Phe Ala Ala Gly Tyr Asn Ala Trp Ile Ala Gln Asn Arg			
	110	115	120
atc acc gac ccc gcc tgc cgg ggc gcg tcc tgg gtg cgc ccg gtg acg			1484
Ile Thr Asp Pro Ala Cys Arg Gly Ala Ser Trp Val Arg Pro Val Thr			
125	130	135	140
gcg ctg gac gtg gcg gcg cgc ggc tac gcg ctg gcg gtg ctc ggc ggc			1532
Ala Leu Asp Val Ala Ala Arg Gly Tyr Ala Leu Ala Val Leu Gly Gly			
	145	150	155
cag ggg cgc ggc atc gac ggc atc acc gcg gca cag ccg ccg acc gcc			1580
Gln Gly Arg Gly Ile Asp Gly Ile Thr Ala Ala Gln Pro Pro Thr Ala			
	160	165	170
gct cct ccg gcg gcc ggg gtc acg ccc gag gag gcg gcg acg gcg gcg			1628
Ala Pro Pro Ala Ala Gly Val Thr Pro Glu Glu Ala Ala Thr Ala Ala			

175	180	185	
gag cgg ctg ctg tcg acg cag aac gcg gac atg ggt tcc aac gcg gtg			1676
Glu Arg Leu Leu Ser Thr Gln Asn Ala Asp Met Gly Ser Asn Ala Val			
190	195	200	
gcc ttc gac ggc tcc acg acg gtg aac ggg cgc ggg ctg ttg ctc ggc			1724
Ala Phe Asp Gly Ser Thr Thr Val Asn Gly Arg Gly Leu Leu Leu Gly			
205	210	215	220
aac ccg cac tac ccg tgg cag ggc gga cgc cgc ttc tgg cag gcg cag			1772
Asn Pro His Tyr Pro Trp Gln Gly Gly Arg Arg Phe Trp Gln Ala Gln			
	225	230	235
cag acg atc ccc ggc gag ctg aac gtg tcg ggc gcg tcc ctg ctg ggc			1820
Gln Thr Ile Pro Gly Glu Leu Asn Val Ser Gly Ala Ser Leu Leu Gly			
	240	245	250
gcg acg acg atc tcg atc ggg cac aac gcc gat gtg gcg tgg agc cat			1868
Ala Thr Thr Ile Ser Ile Gly His Asn Ala Asp Val Ala Trp Ser His			
	255	260	265
acg gtc gcc acg ggc gtc acg ctg aat ctg cat cag ctc agc ctc gat			1916
Thr Val Ala Thr Gly Val Thr Leu Asn Leu His Gln Leu Ser Leu Asp			
	270	275	280
ccg gcc gac ccg acc gtc tat ctg gtg gac ggg aag cgg gag cgg atg			1964
Pro Ala Asp Pro Thr Val Tyr Leu Val Asp Gly Lys Arg Glu Arg Met			
	285	290	295
300			
acg cag cgg acg gtg agc gtc ccg gtg aag ggc ggg gcc gac gtg acc			2012
Thr Gln Arg Thr Val Ser Val Pro Val Lys Gly Gly Ala Asp Val Thr			
	305	310	315
cgc acc cag tgg tgg acc cgc tac ggg ccg gtg gcc acc tcg atg ggc			2060
Arg Thr Gln Trp Trp Thr Arg Tyr Gly Pro Val Ala Thr Ser Met Gly			

320	325	330	
gcg ggg ctg ccg ttg ccg tgg acg gcg agc acg gcg tac gcg ctg aac			2108
Ala Gly Leu Pro Leu Pro Trp Thr Ala Ser Thr Ala Tyr Ala Leu Asn			
335	340	345	
gat ccg aac gcg acg aat ctg cgg atg gcg gac acc ggt ctg ggc ttc			2156
Asp Pro Asn Ala Thr Asn Leu Arg Met Ala Asp Thr Gly Leu Gly Phe			
350	355	360	
ggc aag gcc cgc tcc acg ggt gac gtc gag cgt gcg ctg cac cgg tgc			2204
Gly Lys Ala Arg Ser Thr Gly Asp Val Glu Arg Ala Leu His Arg Ser			
365	370	375	380
cag ggc atg ccg tgg gtg aac acg atc gcg gcg gac cgg gcg ggt cgc			2252
Gln Gly Met Pro Trp Val Asn Thr Ile Ala Ala Asp Arg Ala Gly Arg			
385	390	395	
tgc ttc ttc gcg cag tgc cag gtg ctg ccg agg atc acc gac gcg ttg			2300
Ser Phe Phe Ala Gln Ser Gln Val Leu Pro Arg Ile Thr Asp Ala Leu			
400	405	410	
gcg gag cgc tgc tgc acc ccg ctg ggc cgg gcc acc tac ccc gct tcc			2348
Ala Glu Arg Cys Ser Thr Pro Leu Gly Arg Ala Thr Tyr Pro Ala Ser			
415	420	425	
ggc ctc gcg gtg ctg gac ggt tgc cgg acg gac tgc gcg ctg ggc agc			2396
Gly Leu Ala Val Leu Asp Gly Ser Arg Thr Asp Cys Ala Leu Gly Ser			
430	435	440	
gac ccg gac gcg gtg cgg ccg ggg atc ttc ggc ccg ggc cgg atg ccg			2444
Asp Pro Asp Ala Val Arg Pro Gly Ile Phe Gly Pro Gly Arg Met Pro			
445	450	455	460
gtg ctg aag aac cag ccg tac gtg gag aac tcc aac gac agc gcg tgg			2492
Val Leu Lys Asn Gln Pro Tyr Val Glu Asn Ser Asn Asp Ser Ala Trp			

465	470	475	
ctg acc aat gcg gag cgg ccg ctg acc ggg tac gag cgg gtc ttc ggc			2540
Leu Thr Asn Ala Glu Arg Pro Leu Thr Gly Tyr Glu Arg Val Phe Gly			
480	485	490	
acg atc gcg acg ccc cgg tcg atg cgg acg cgc ggc gcg atc gag gac			2588
Thr Ile Ala Thr Pro Arg Ser Met Arg Thr Arg Gly Ala Ile Glu Asp			
495	500	505	
gtc gcg tcg atg gcg gac cgg ggc cgc ctc cgg gtc ggg gac ctt cag			2636
Val Ala Ser Met Ala Asp Arg Gly Arg Leu Arg Val Gly Asp Leu Gln			
510	515	520	
cgg cag cag ttc gcc aac cgt gcg ccg gcc ggg gat ctg gcc gcc tcc			2684
Arg Gln Gln Phe Ala Asn Arg Ala Pro Ala Gly Asp Leu Ala Ala Ser			
525	530	535	540
gag gcc gcc aag tgg tgt gcg gcg ctg ccg ggc ggc acg gcc gtg ggc			2732
Glu Ala Ala Lys Trp Cys Ala Ala Leu Pro Gly Gly Thr Ala Val Gly			
545	550	555	
tcc gac gga acg ccg gtc gac gtg tcg gcg gcc tgc cgg gtg ctg cgg			2780
Ser Asp Gly Thr Pro Val Asp Val Ser Ala Ala Cys Arg Val Leu Arg			
560	565	570	
cgc tgg gac cgg acc gtg gac agc gac agc cgg ggc gcg ctg ctc ttc			2828
Arg Trp Asp Arg Thr Val Asp Ser Asp Ser Arg Gly Ala Leu Leu Phe			
575	580	585	
gac cgg ttc tgg cgg aag gcg tcg tcg gcg ccc gcc gcc gag ctg tgg			2876
Asp Arg Phe Trp Arg Lys Ala Ser Ser Ala Pro Ala Ala Glu Leu Trp			
590	595	600	
agg acg ccg ttc gat ccg gcc gac ccg gtg cgc act ccg cgc ggc ctg			2924
Arg Thr Pro Phe Asp Pro Ala Asp Pro Val Arg Thr Pro Arg Gly Leu			

605	610	615	620	
aac acg gcc gcg ccc gtc ctg ggc agg gcc ctg gcg gac gcc gtg gcg				2962
Asn Thr Ala Ala Pro Val Leu Gly Arg Ala Leu Ala Asp Ala Val Ala				
625	630	635		
gag ctg cgg gcg gcg ggc atc gcg ctg gac gcc ccg ctg ggc gag cac				3020
Glu Leu Arg Ala Ala Gly Ile Ala Leu Asp Ala Pro Leu Gly Glu His				
640	645	650		
cag ttc gtc gtg cgg aac ggc aag cgg ctc ccg atc ggc ggc ggg acg				3068
Gln Phe Val Val Arg Asn Gly Lys Arg Leu Pro Ile Gly Gly Gly Thr				
655	660	665		
gag tcg ctg ggc atc tgg aac aag acc gag ccg cag tgg aac gcg gcg				3116
Glu Ser Leu Gly Ile Trp Asn Lys Thr Glu Pro Gln Trp Asn Ala Ala				
670	675	680		
ggc ggc ggc tat acg gag gtg tcg tcg ggc tcc agc tac atc cag gcg				3164
Gly Gly Gly Tyr Thr Glu Val Ser Ser Gly Ser Ser Tyr Ile Gln Ala				
685	690	695	700	
gtc ggc tgg gac gac agc cgc tgc ccg gtg gcc cgg acg ctg ctg acg				3212
Val Gly Trp Asp Asp Ser Arg Cys Pro Val Ala Arg Thr Leu Leu Thr				
705	710	715		
tac tcc cag tcg gag aac ccg aag tca ccg cac tac agc gac cag acc				3260
Tyr Ser Gln Ser Glu Asn Pro Lys Ser Pro His Tyr Ser Asp Gln Thr				
720	725	730		
agg ctg tac gcg ggt gag cgc tgg gtg acg tcc cgg ttc tgc gag agg				3308
Arg Leu Tyr Ala Gly Glu Arg Trp Val Thr Ser Arg Phe Cys Glu Arg				
735	740	745		
gac atc gcg cgt tcg ccg gac ctg cgg gtg gtg cgg gtg cac gag cgg				3356
Asp Ile Ala Arg Ser Pro Asp Leu Arg Val Val Arg Val His Glu Arg				

750	755	760	
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Arg			
765			
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 tcc 5692

<210> 2

<211> 765

<212> PRT

<213> Streptomyces Sp.

<400> 2

Leu Thr Leu Arg Asn Arg Leu Arg Leu Leu Gly Val Ala Gly Leu Ala

-35

-30

-25

Leu Phe Thr Val Ser Ala Ser Leu Pro Pro Ala Thr Ala Ser Gly Thr

-20

-15

-10

Gln Glu Thr Arg His Pro Ser Gly Ser Gly Leu Ser Ala Val Ile Arg

-5	1	5
Tyr Thr Glu Tyr Gly Ile Pro His Ile Val Ala Glu Asp Tyr Ala Gln		
10	15	20 25
Leu Gly Phe Gly Thr Gly Trp Ala Gln Ala Ala Asp Gln Val Cys Thr		
	30	35 40
Leu Ala Asp Gly Phe Leu Thr Val Arg Gly Glu Arg Ser Arg Phe Phe		
	45	50 55
Gly Pro Asp Ala Ala Thr Asp Tyr Ser Leu Ser Ser Ala Ala Thr Asn		
	60	65 70
Leu Ser Ser Asp Leu Tyr Phe Arg Gly Val Arg Asp Ser Gly Thr Val		
	75	80 85
Glu Lys Leu Leu Lys Glu Pro Ala Pro Ala Gly Pro Ser Arg Asp Val		
	90	95 100 105
Lys Glu Thr Met Arg Gly Phe Ala Ala Gly Tyr Asn Ala Trp Ile Ala		
	110	115 120
Gln Asn Arg Ile Thr Asp Pro Ala Cys Arg Gly Ala Ser Trp Val Arg		
	125	130 135
Pro Val Thr Ala Leu Asp Val Ala Ala Arg Gly Tyr Ala Leu Ala Val		
	140	145 150
Leu Gly Gly Gln Gly Arg Gly Ile Asp Gly Ile Thr Ala Ala Gln Pro		
	155	160 165
Pro Thr Ala Ala Pro Pro Ala Ala Gly Val Thr Pro Glu Glu Ala Ala		
	170	175 180 185
Thr Ala Ala Glu Arg Leu Leu Ser Thr Gln Asn Ala Asp Met Gly Ser		
	190	195 200
Asn Ala Val Ala Phe Asp Gly Ser Thr Thr Val Asn Gly Arg Gly Leu		
	205	210 215

Leu Leu Gly Asn Pro His Tyr Pro Trp Gln Gly Gly Arg Arg Phe Trp  
 220 225 230  
 Gln Ala Gln Gln Thr Ile Pro Gly Glu Leu Asn Val Ser Gly Ala Ser  
 235 240 245  
 Leu Leu Gly Ala Thr Thr Ile Ser Ile Gly His Asn Ala Asp Val Ala  
 250 255 260 265  
 Trp Ser His Thr Val Ala Thr Gly Val Thr Leu Asn Leu His Gln Leu  
 270 275 280  
 Ser Leu Asp Pro Ala Asp Pro Thr Val Tyr Leu Val Asp Gly Lys Arg  
 285 290 295  
 Glu Arg Met Thr Gln Arg Thr Val Ser Val Pro Val Lys Gly Gly Ala  
 300 305 310  
 Asp Val Thr Arg Thr Gln Trp Trp Thr Arg Tyr Gly Pro Val Ala Thr  
 315 320 325  
 Ser Met Gly Ala Gly Leu Pro Leu Pro Trp Thr Ala Ser Thr Ala Tyr  
 330 335 340 345  
 Ala Leu Asn Asp Pro Asn Ala Thr Asn Leu Arg Met Ala Asp Thr Gly  
 350 355 360  
 Leu Gly Phe Gly Lys Ala Arg Ser Thr Gly Asp Val Glu Arg Ala Leu  
 365 370 375  
 His Arg Ser Gln Gly Met Pro Trp Val Asn Thr Ile Ala Ala Asp Arg  
 380 385 390  
 Ala Gly Arg Ser Phe Phe Ala Gln Ser Gln Val Leu Pro Arg Ile Thr  
 395 400 405  
 Asp Ala Leu Ala Glu Arg Cys Ser Thr Pro Leu Gly Arg Ala Thr Tyr  
 410 415 420 425  
 Pro Ala Ser Gly Leu Ala Val Leu Asp Gly Ser Arg Thr Asp Cys Ala

430	435	440
Leu Gly Ser Asp Pro Asp Ala Val Arg Pro Gly Ile Phe Gly Pro Gly		
445	450	455
Arg Met Pro Val Leu Lys Asn Gln Pro Tyr Val Glu Asn Ser Asn Asp		
460	465	470
Ser Ala Trp Leu Thr Asn Ala Glu Arg Pro Leu Thr Gly Tyr Glu Arg		
475	480	485
Val Phe Gly Thr Ile Ala Thr Pro Arg Ser Met Arg Thr Arg Gly Ala		
490	495	500
Ile Glu Asp Val Ala Ser Met Ala Asp Arg Gly Arg Leu Arg Val Gly		
510	515	520
Asp Leu Gln Arg Gln Gln Phe Ala Asn Arg Ala Pro Ala Gly Asp Leu		
525	530	535
Ala Ala Ser Glu Ala Ala Lys Trp Cys Ala Ala Leu Pro Gly Gly Thr		
540	545	550
Ala Val Gly Ser Asp Gly Thr Pro Val Asp Val Ser Ala Ala Cys Arg		
555	560	565
Val Leu Arg Arg Trp Asp Arg Thr Val Asp Ser Asp Ser Arg Gly Ala		
570	575	580
Leu Leu Phe Asp Arg Phe Trp Arg Lys Ala Ser Ser Ala Pro Ala Ala		
590	595	600
Glu Leu Trp Arg Thr Pro Phe Asp Pro Ala Asp Pro Val Arg Thr Pro		
605	610	615
Arg Gly Leu Asn Thr Ala Ala Pro Val Leu Gly Arg Ala Leu Ala Asp		
620	625	630
Ala Val Ala Glu Leu Arg Ala Ala Gly Ile Ala Leu Asp Ala Pro Leu		
635	640	645

Gly Glu His Gln Phe Val Val Arg Asn Gly Lys Arg Leu Pro Ile Gly  
 650                      655                      660                      665  
 Gly Gly Thr Glu Ser Leu Gly Ile Trp Asn Lys Thr Glu Pro Gln Trp  
                     670                      675                      680  
 Asn Ala Ala Gly Gly Gly Tyr Thr Glu Val Ser Ser Gly Ser Ser Tyr  
                     685                      690                      695  
 Ile Gln Ala Val Gly Trp Asp Asp Ser Arg Cys Pro Val Ala Arg Thr  
                     700                      705                      710  
 Leu Leu Thr Tyr Ser Gln Ser Glu Asn Pro Lys Ser Pro His Tyr Ser  
                     715                      720                      725  
 Asp Gln Thr Arg Leu Tyr Ala Gly Glu Arg Trp Val Thr Ser Arg Phe  
 730                      735                      740                      745  
 Cys Glu Arg Asp Ile Ala Arg Ser Pro Asp Leu Arg Val Val Arg Val  
                     750                      755                      760  
 His Glu Arg Arg

765

<210> 3

<211> 20

<212> PRT

<213> Streptomyces Sp.

<400> 3

Ser Asn Ala Val Ala Phe Asp Gly Ser Thr Thr Val Asn Gly Arg Gly  
 1                      5                      10                      15

Leu Leu Leu Gly  
 20

<210> 4

<211> 20

<212> PRT

<213> Streptomyces Sp.

<400> 4

Gly Ser Gly Leu Ser Ala Val Ile Arg Tyr Thr Glu Tyr Gly Ile Pro

1 5 10 15

His Ile Val Ala

20

<210> 5

<211> 20

<212> PRT

<213> Streptomyces Sp.

<400> 5

Gly Ser Gly Leu Ser Ala Val Ile Arg Tyr Thr Glu Tyr Gly Ile Pro

1 5 10 15

His His Val Ala

20

<210> 6

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide designed to act as PCR primer (forward) to amplify the DNA coding N-terminal amino acid sequences of FR901379 acyrase small subunit.

<400> 6

ctstcsgcsg tsatc

15

<210> 7

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide designed to act as PCR primer (reverse) to amplify the DNA coding N-terminal amino acid sequences of FR901379 acyrase small subunit.

<400> 7

gtggtgsggg atsc

15

<210> 8

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide designed to act as PCR primer (forward) to amplify the DNA coding N-terminal amino acid sequences of FR901379 acyrase large subunit.

<400> 8

csgtsgcstt cgacgg

16

<210> 9

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide designed to act as PCR primer (reverse) to amplify the DNA coding N-terminal amino acid sequences of FR901379 acyrase large subunit.

<400> 9

sccsagsags agscc

15

<210> 10

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide designed to act as PCR primer (forward) to amplify the DNA coding sequence between FR901379 acyrase small subunit and large subunit.

<400> 10

atccggtaca cggagtacgg

20

<210> 11

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide designed to act as PCR primer (reverse) to amplify the DNA coding sequence between FR901379 acyrase small subunit



and large subunit.

<400> 11

cgttcacccgt cgtggagcc

19

<210> 12

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide designed for use in changing site from EcoR I site to Sac I site.

<400> 12

aattgagctc

10

<210> 13

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide designed to act as sequencing primer.

<400> 13

caactgcgcg tagtcc

16

<210> 14

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide designed to act as sequencing primer.

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16

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cagttccgcc tcgtcg

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16

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16

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ggcggatgatg aagtcg

16

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cgacttcac accgcc

16

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ggcgacttct tcaccg

16

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cggtgaagaa gtcgcc

16

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<400> 57

ccagacgggtt gacagc

16